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GERMcode: A Stochastic Model for Space Radiation Risk Assessment

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A new computer model, the GCR Event-based Risk Model code (GERMcode), was developed to describe biophysical events from high-energy protons and high charge and energy (HZE) particles that have been studied at the NASA Space Radiation Laboratory (NSRL) for the purpose of simulating space radiation biological effects. In the GERMcode, the biophysical description of the passage of HZE particles in tissue and shielding materials is made with a stochastic approach that includes both particle track structure and nuclear interactions. The GERMcode accounts for the major nuclear interaction processes of importance for describing heavy ion beams, including nuclear fragmentation, elastic scattering, and knockout-cascade processes by using the quantum multiple scattering fragmentation (QMSFRG) model. The QMSFRG model has been shown to be in excellent agreement with available experimental data for nuclear fragmentation cross sections. For NSRL applications, the GERMcode evaluates a set of biophysical properties, such as the Poisson distribution of particles or delta-ray hits for a given cellular area and particle dose, the radial dose on tissue, and the frequency distribution of energy deposition in a DNA volume. By utilizing the ProE/Fishbowl ray-tracing analysis, the GERMcode will be used as a bi-directional radiation transport model for future spacecraft shielding analysis in support of Mars mission risk assessments.

Recent radiobiological experiments suggest the need for new approaches to risk assessment that include time-dependent biological events due to the signaling times for activation and relaxation of biological processes in cells and tissue. Thus, the tracking of the temporal and spatial distribution of events in tissue is a major goal of the GERMcode in support of the simulation of biological processes important in GCR risk assessments. In order to validate our approach, basic radiobiological responses such as cell survival curves, mutation, chromosomal aberrations, and representative mouse tumor induction curves are implemented into the GERMcode. Extension of these descriptions to other endpoints related to non-targeted effects and biochemical pathway responses will be discussed.